REMARKS

1. STATUS OF THE SPECIFICATION

The Specification has been amended to delete embedded hyperlink in conformance with the Examiner's request[1] and in compliance with MPEP § 608.01.

2. STATUS OF THE CLAIMS

Claims 1-16 are pending.

Claims 3 and 11-13 have previously been withdrawn as directed to a non-elected invention.

Claim 1 has been amended to recite that the DNA sequence is "isolated." Support is in the Specification's teaching ". . . cDNAs encoding the proteins of the present invention were successfully **isolated** from rice cDNA libraries based on this amino acid sequence information."[2]

Claims 1, 2, 4, 5, and 10 have been amended by changing "DNA" to "DNA sequence" to further clarify that the molecule contains more than one nucleotide.

Claim 1 has also been amended by canceling the recitation of (b) through (d) since these elements are now recited in new claims 17-42.

Claim 1 has also been amended to recite that the DNA sequence that encodes SEQ ID NO:3 "lacks a nucleotide sequence that encodes an amino acid sequence from amino acid 1 to amino acid 28 of SEQ ID NO:2." Support is in the specification's teaching that "The nucleotide sequence of the cDNA of the elicitor-binding protein of the present invention is presented in SEQ ID NO: 1, and SEQ ID NO: 2 shows the amino acid sequence of the protein encoded by this cDNA. Moreover, the nucleotide sequence of the DNA in which the portion encoding a signal peptide has been removed from the cDNA is shown in SEQ ID NO: 3, and the amino acid sequence of the protein encoded by this DNA is presented in SEQ ID NO: 4."[3]

Claim 5 has been amended for further clarity by changing "that carries" to "comprising."

Claims 6, 10 and 14 have been amended (and new claims 17-42 have been added) to recite that the "plant transformant has increased resistance to disease compared to a plant lacking

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1 Office Action, page 2, 5th paragraph.
2 (Emphasis added) Specification, page 3, lines 12-14.
3 Specification, page 6, lines 6-11.

said DNA sequence." Support is in the Specification's teaching that the invention "is considered to contribute to the development of breeds of crops that are **resistant to diseases** and novel disease control technologies."[4] "Since these elicitors induce resistance to blast in rice, the proteins of the present invention can be applied to the **development of novel disease control** technologies."[5]

Claim 10 has been amended by changing "the" plant transformant to "a" plant transformant" to avoid potential lack of antecedent basis. Claim 10 has also been amended by adding "to produce a transformed plant cell" to provide antecedent basis for the newly added recitation of "wherein said plant transformant has increased resistance to disease compared to a plant lacking said DNA sequence."

Claim 14 has been amended by canceling "the protein of claim 3" and replacing it with "the DNA sequence of claim 1" to avoid potentially reciting a non-elected invention.

New Claims 17-24 recite "SEQ ID NO:1" are supported by originally filed Claims 1(a), 6-10 and 14-16.

New Claims 25-33 recite a DNA sequence encoding a protein that has "from 95% to 100% identity with the amino acid sequence of SEQ ID NO:2" and has "binding activity to a chitin oligosaccharide elicitor." Support is in original Claims 1(c) and (d), 6-10 and 14-16. Additional support for the percent identities is in the Specification's teaching that "'High homology' with the full length amino acid sequence means a sequence identity of at least 35%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 98% or more."[6]

New Claims 34-42 recite a DNA sequence encoding a protein that has "from 95% to 100% identity with the amino acid sequence of SEQ ID NO:4" and has "binding activity to a chitin oligosaccharide elicitor." Support is in original Claims 1(c) and (d), 6-10 and 14-16. Additional support is in the Specification's teaching that is discussed in the immediate prior paragraph.

Claim amendments were made to describe particular embodiments of the invention, notwithstanding Applicants' belief that the cancelled and unamended claims would have been allowable, without acquiescing to any of the Examiner's arguments, and

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4 (Emphasis added) Specification, page 22, lines 7-8.
5 (Emphasis added) Specification, page 31, lines 11-13.
6 Specification, page 6, lines 35-36.

without waiving the right to prosecute the unamended (or similar) claims in another application, but rather for the purpose of furthering Applicants' business goals and expediting the patent application process in a manner consistent with the PTO's Patent Business Goals (PBG).[7]

3. ELECTION

Applicants affirm their election, without traverse, of Group I, Claims 1-2, 4-10 and 14-16, "drawn to a DNA encoding a protein having elicitor binding activity, a vector and a plant/seed comprising said DNA, and a plant transformation method."

4. OBJECTION TO CLAIMS 14-16

The Examiner objected to Claims 14-16 "for depending upon the non-elected invention, claim 3."[8] Independent Claim 14 has been amended to depend from elected Claim 1, thereby obviating this objection.

The Examiner suggested amending Claim 1 for clarification by inserting "An isolated" before "DNA." Applicants have made this amendment.

5. REEJCTION OF CLAIMS 1-2, 4-10 AND 14-16 UNDER 35 U.S.C. §112, FIRST PARAGRAPH (ENABLEMENT)

The Examiner rejected Claims 1-2, 4-10 and 14-16 under 35 U.S.C. §112, first paragraph, for alleged non-enablement.[9] Applicants respectfully disagree, as discussed below.

A. Claims 1-2, 4-10, 14-16

The Examiner admitted that the Specification is "enabling for an isolated DNA encoding **SEQ ID NO: 2 or 4**, or the DNA sequence of **SEQ ID NO: 1 or 3**, a vector comprising said DNA sequence, a transgenic plant comprising said DNA sequence or vector and a method for transforming a plant with said DNA sequence."[10] Accordingly, amended Claims 1-2, 4-10, 14-16 that recite **SEQ ID NO:3** are **admittedly enabled**.

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7 65 Fed. Reg. 54603 (September 8, 2000).
8 Office Action, page 2, penultimate paragraph.
9 Office Action, page 3, 2nd paragraph.
10 *Id.*

B. New Claims 17-24

In view of the Examiner's above statement in item 5.A., new Claims 17-24 that recite **SEQ ID NO:1** are **admittedly enabled.**

C. New Claims 25-33

In view of the Examiner's above statement in item 5.A., new Claim 26 that recites "100% identity" with **SEQ ID NO:2** is **admittedly enabled.**

New Claims 25 and 27-33 recite "from 95% to 100% identity" with SEQ ID NO:2. Methods for **making** sequences that fall within this range of homology is within the skill in the art, as admitted by the Examiner, who recognized that "mutagenesis techniques are known."[11] Methods for **using** these sequences, such as for producing plant transformants,[12] for producing CEBiP proteins,[13] and for preparing antibodies that bind to CEBiP proteins[14]are taught in the Specification. Since methods for making and using the sequences recited in Claims 25 and 27-33 are taught by the Specification, these claims are enabled.

D. New Claims 34-42

In view of the Examiner's above statement in item 5.A., new Claim 35 that recites "100% identity" with **SEQ ID NO:4** is **admittedly enabled**.

New Claims 34 and 36-42 recite "from 95% to 100% identity" with SEQ ID NO:4. Since methods for **making** and **using** the sequences recited in Claims 34 and 36-42 are taught by the Specification (as discussed in item 5.D., *supra*), these claims are enabled.

6. REJECTION OF CLAIMS 1-2, 4-10 AND 14-16 UNDER 35 U.S.C. §112, FIRST PARAGRAPH (WRITTEN DESCRIPTION)

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11 Office Action, page 5, 1st paragraph.
12 Specification, page 8, line 16 to page 9, line 2; page 10, line 2 to page 11, line 30; Example 8, beginning on page 22.
13 Specification, page 9, lines 3-27.
14 Specification, paragraph bridging pages 9-10.

Claims 1-2, 4-10 and 14-16 stand rejected under 35 U.S.C. §112, first paragraph, for allegedly lacking adequate written description support. Applicants respectfully traverse, as discussed below.

A. Claims 1-2, 4-10, 14-16

The Examiner admitted that Applicants "describes the isolated DNA sequence of **SEQ ID NO: 1 or 3** encoding **SEQ ID NO:2 or 4**, a vector comprising said DNA sequence, transformed plant, plant cell or seed comprising said DNA sequence, and a method of transforming transforming plants with said DNA sequence."[15] Accordingly, amended Claims 1-2, 4-10, 14-16 that recite **SEQ ID NO:3** are **admittedly supported by an adequate written description.**

B. New Claims 17-24

In view of the Examiner's above statement in item 6.A., new Claims 17-24 that recite **SEQ ID NO:1** are **admittedly supported by an adequate written description.**

C. New Claim 26

New Claim 26 recites a DNA sequence encoding a protein that has "100% identity" with the amino acid sequence of **SEQ ID NO:2**. The genus of DNA sequences of Claim 26 enjoys adequate written description support because the genetic code is widely known. In this regard, the Examiner's attention is respectfully drawn to MPEP 2163, which says

> "Description of a representative number of species does not require the description to be of such specificity that it would provide individual support for each species that the genus embraces. For example, in the molecular biology arts, if an applicant disclosed **an amino acid sequence**, it would be **unnecessary** to provide an **explicit disclosure of nucleic acid sequences** that encoded the amino acid sequence. Since the genetic code is widely known, a disclosure of **an amino acid sequence** would provide sufficient information such that one would accept that an applicant was in possession of the **full genus of nucleic acids** encoding a

15 *Id.*

given amino acid sequence."[16]

Accordingly, new Claim 26 meets the requirements for written description.

D. New Claim 35

New Claim 35 recites a DNA sequence encoding a protein that has "100% identity" with the amino acid sequence of **SEQ ID NO:4**. The genus of DNA sequences of Claim 35 is adequately described for the same reasons discussed in item 6.C., *supra*.

7. REJECTION OF CLAIMS 1-2, 4-10 AND 14-16 UNDER 35 U.S.C. § 102(b) OVER YANO *et al.*

Claims 1-2, 4-10 and 14-16 were rejected under 35 U.S.C. § 102(b) for alleged anticipation by Yano *et al.* (U.S. Patent No. 6,274,789).[17] Applicants respectfully disagree because Yano *et al.* does not disclose all the limitations of the claims.

Yano *et al.* discloses DNA SEQ ID NO:2 (3925 na) and SEQ ID NO:3 (10322 na). Alignment of Yano *et al.*'s sequences with the recited SEQ ID NOs: 1-4 is shown in Tab 1. The alignment shows that Yano *et al.*'s DNA SEQ ID NO:2 (3925 na) and SEQ ID NO:3 (10322 na) have 36.2% and 36.0% identity with the recited SEQ ID NO:1, respectively. Each of Yano *et al.*'s DNA SEQ ID NO:2 and SEQ ID NO:3 have 41.3% identity with the recited SEQ ID NO:3. Yano *et al.* also discloses amino acid sequence SEQ ID NO:1 (1205 aa) that has 18.8% identity with each of the recited SEQ ID NO:2 and SEQ ID NO:4.

Based on the above % identities, Yano *et al.* does not disclose (a) SEQ ID NO:3 that is recited in Claims 1-2, 4-10 and 14-16, (b) SEQ ID NO:1 that is recited in new Claims 17-24, (c) a protein that has from 95% to 100% identity with SEQ ID NO:2, as recited in new Claims 25-33, and (d) a protein that has from 95% to 100% identity with SEQ ID NO:4, as recited in new Claims 34-42. Accordingly, Yano *et al.* cannot anticipate any of these claims.

Accordingly, Applicants respectfully request withdrawal of the rejection of Claims 1-2, 4-10 and 14-16 under 35 U.S.C. § 102(b), and also assert that new Claims 17-42 are novel.

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16 Emphasis added.

17 Yano *et al.* was issued on August 14, 2001, was filed on June 11, 1999, and claims priority to a Japanese patent application filed June 12, 1998.

8. REJECTION OF CLAIMS 1-2, 4-10 AND 14-16 UNDER 35 U.S.C. § 102(e) OVER LaROSA *et al.*

Claims 1-2, 4-10 and 14-16 were rejected under 35 U.S.C. § 102(e) for alleged anticipation by LaRosa *et al.* (U.S. Patent Application No. 20040123343).[18] Applicants respectfully disagree because LaRosa *et al.* does not disclose all the claims' limitations, and is not enabled. This is further discussed below.

A. LaRosa *et al.* does not disclose all the claims' limitations

Amended Claims 1-2, 4-10 and 14-16, and new Claims 34-42 recite an isolated DNA sequence that "lacks a nucleotide sequence that encodes an amino acid sequence from amino acid 1 to amino acid 28 of SEQ ID NO:2." However, LaRosa *et al.* does **not** disclose this limitation. Rather LaRosa *et al.* discloses SEQ ID NO:2, which **contains** amino acid 1 to amino acid 28. Accordingly, LaRosa *et al.* does not anticipate Claims 1-2, 4-10 and 14-16 and new Claims 34-42.

B. LaRosa *et al.* is not enabled

LaRosa *et al.* lacks an enabling disclosure of amended Claims 6-10 and 14-16, and of new Claims 17-42 because it fails to enable one of skill in the art to select the recited sequences to produce a plant that has the recited "increased resistance to disease." Under the law,

> ". . . anticipation requires that the assertedly anticipatory disclosure enabled the subject matter of the reference and thus of the patented invention without undue experimentation."[19]

LaRosa *et al.* discloses a 1399 base pair sequence with 100% identity to SEQ ID NO:1.[20] Importantly, however, LaRosa *et al.* discloses that its 1399 bp sequence is **just one among 102,483 DNA sequences**[21] that may be used to produce "transgenic plants having at least one

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18 LaRosa *et al.* was filed on May 14, 2003.

19 Elan Pharmaceuticals, Inc. v. Mayo Foundation for Medical Education and Research, Fed. Cir., No. 00-1467, 10/2/03; See also Akzo N.V. v. U.S. Intern. Trade Com'n, 808 F.2d 1471 (Fed. Cir. 1986) citing In re Brown, 329 F.2d 1006, 1011, 141 USPQ 245, 249 (CCPA 1964) ("Under 35 U.S.C. ' 102 . . . the prior art reference must be enabling, thus placing the allegedly disclosed matter in the possession of the public.")

20 Office Action, page 10, 2nd paragraph.

21 LaRosa *et al.*, paragraph [0005].

improved property"[22] including **(1)** improved yield resulting from improved utilization of nitrogen, **(2)** improved yield resulting from improved utilization of phosphorous, **(3)** improved yield resulting from improved utilization of carbohydrate, **(4)** improved yield resulting from improved response to cold, **(5)** improved yield resulting from improved response to heat, **(6)** improved yield resulting from improved response to drought, **(7)** improved yield resulting from improved response to salt, **(8)** improved yield resulting from improved response to attack by pests or pathogens, **(9)** improved growth, **(10)** improved development, **(11)** increased yield as the result of modified expression of plant growth regulators, **(12)** increased yield as the result of modification of cell cycle, **(13)** increased yield as the result of modified photosynthesis pathways, **(14)** modified flavonoid content, **(15)** modified seed oil, **(16)** modified protein quantity, **(17)** modified protein quality, **(18)** modified herbicide tolerance, **(19)** modified rate of homologous recombination,[23] **(19)** yield improvement by improved nitrogen flow, sensing, uptake, storage and/or transport,24 **(20)** yield improvement by effects on carbohydrate metabolism by increased sucrose production, **(21)** yield improvement by effects on carbohydrate metabolism by increased sucrose transport,[25] **(22)** yield improvement resulting from increased photosynthesis,[26] **(23)** yield improvement resulting from increased phosphorus uptake, transport or utilization,[27] **(24)** yield improvement resulting from improved plant growth and development by helping plants to tolerate stressful growth conditions,[28] **(25)** improved tolerance to cold or freezing temperatures,[29] **(26)** improved tolerance to heat,[30] **(27)** improved tolerance to extreme osmotic conditions,[31] **(28)** improved tolerance to drought conditions,[32] **(29)** improved tolerance to effects of plant pests or pathogens,[33] **(30)** manipulating growth rate and quality traits,[34] **(31)** increased seed protein quantity and/or quality,[35] **(32)** increased seed oil quantity and/or quality,[36] **(33)**

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22 LaRosa *et al.*, paragraph [0015].
23 LaRosa *et al.*, paragraph [0020].
24 LaRosa *et al.*, paragraph [0037].
25 LaRosa *et al.*, paragraph [0038].
26 LaRosa *et al.*, paragraph [0039].
27 LaRosa *et al.*, paragraph [0040].
28 LaRosa *et al.*, paragraph [0041].
29 LaRosa *et al.*, paragraph [0042].
30 LaRosa *et al.*, paragraph [0043].
31 LaRosa *et al.*, paragraph [0044].
32 LaRosa *et al.*, paragraph [0045].
33 LaRosa *et al.*, paragraph [0046].
34 LaRosa *et al.*, paragraph [0047].
35 LaRosa *et al.*, paragraph [0048].

improved disease responses,[37] **(34)** increased and/or modified reserve polysaccharides for use in food, pharmaceutical, cosmetic, paper and paint industries, **(35)** modification of flavonoid/isoflavonoid metabolism,[38] **(36)** altered morphologies and improved plant growth and development profiles,[39] **(37)** improved tolerance to plant herbicides,[40] **(38)** altered transcription factors in plants,[41] **(39)** increased rate of homologous recombination,[42] and **(40)** altered lignin biosynthesis.[43]

LaRosa *et al.* also discloses that one or more of the above-listed **at least forty functions** may be possessed by not only one or more of its 102,483 DNA sequences, but also by one or more of the DNA sequences that encode "**functional homologs**" that **(a)** "differ in one or more amino acids,"[44] **(b)** have the same function,[45] **(c)** have increased activity, [46] **(d)** have decreased activity,[47] **(e)** have "altered specificity,"[48] or **(f)** have "at least about 35% sequence identity."[49]

Importantly, however, LaRosa *et al.* does not provide **any data or guidance** on which of the **102,483 DNA sequences** correlates with which of the above-listed **at least forty functions**.

Nor does LaRosa *et al.* provide **any data or guidance** on **which of the innumerable modifications** (including deletions, additions, and/or substitutions) would produce the equally **innumerable "functional homologs**" that are encoded encoded by the 102,483 DNA sequences, and that also (a) have the same function, (b) have increased activity, (d) have decreased activity, and/or (e) have "altered specificity."

Indeed, one need go no farther than the Examiner's statements in the instant Office Action that confirm the non-enablement of LaRosa *et al.*'s disclosure:50

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36 LaRosa *et al.*, paragraph [0049].
37 LaRosa *et al.*, paragraph [0050].
38 LaRosa *et al.*, paragraph [0052].
39 LaRosa *et al.*, paragraph [0053].
40 LaRosa *et al.*, paragraph [0054].
41 LaRosa *et al.*, paragraph [0055].
42 LaRosa *et al.*, paragraph [0056].
43 LaRosa *et al.*, paragraph [0057].
44 LaRosa *et al.*, paragraph [0062].
45 *Id.*
46 LaRosa *et al.*, paragraph [0063].
47 *Id.*
48 *Id..*
49 LaRosa *et al.*, paragraph [0064].
50 Applicants' incorporation of the Examiner's argument is made without acquiescing to it with respect to Applicants' claimed invention.

> "[I]t is **not routine** in the art to screen for multiple substitutions or multiple modifications . . . One skilled in the art would expect any tolerance to modification for a given DNA/protein to diminish with each further and additional modification or multiple substitutions/deletions. One skilled in the art would have to **make all possible nucleotide substitutions and deletions** in . . . [LaRosa *et al.*'s **102,483 DNA sequences** and in each of the DNA sequences that encode a **multitude of functional homologs** that (a) "differ in one or more amino acids," (b) have the same function, (c) have increased activity, (d) have decreased activity, (e) have "altered specificity," or (f) have "at least about 35% sequence identity"] and **test** all nucleotide sequences that meet the structural limitations to determine which also meet the functional limitation [of one or more of above-listed **at least forty functions**]. One would also have to test and evaluate pathogen resistance activity of the DNA sequences in a transgenic plant."[51]

Said differently, based on the paucity of guidance in LaRosa *et al.*, one of skill in the art would have more success in picking a needle in a haystack than in **selecting**, from LaRosa's innumerable number of sequences, the recited SEQ ID NO:3 that "lacks a nucleotide sequence that encodes an amino acid sequence from amino acid 1 to amino acid 28 of SEQ ID NO:2" (Claims 6-16), the recited SEQ ID NO:1 (Claims 17-24), the recited SEQ ID NO:2 (Claims 25-33), and the recited SEQ ID NO:4 (claims 34-42), **and correlating** expression of each of these sequences with the recited **function** of conferring "increased resistance to disease." It would require undue experimentation to make this determination based on LaRosa's disclosure. Thus, LaRosa *et al.*'s disclosure is non-enabling of the claims. It therefore cannot anticipate them.

Since LaRosa *et al.* fails to disclose all the limitations of the claims and is non-enabling, Applicants respectfully request withdrawal of the rejection of Claims 1-2, 4-10 and 14-16 under 35 U.S.C. § 102(e), and also aver that new Claims 17-42 are novel.

CONCLUSION

Applicants respectfully request reconsideration of the application in view of the above, which places the claims in condition for allowance. To expedite prosecution, Applicants also

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51 (Emphasis added) Office Action, page 5, 1st paragraph. The Examiner's statements have been edited to change reference from Applicant's SEQ ID NO:1 to LaRosa *et al.*'s multitude sequences.

respectfully invite the Examiner to **call the undersigned before drafting another written communication**, if any.

Respectfully submitted,

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